

Amendments to the Claims

The listing of the claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

Claim 1 (Previously Presented): A homoserine transsuccinylase which possesses at least one mutation as compared with a homoserine transsuccinylase wild-type enzyme and exhibits a reduced sensitivity toward L-methionine or SAM as compared with the wild-type enzyme, with the wild-type enzyme possessing an amino acid sequence which comprises a constituent sequence AspGlyXaaXaaXaaThrGlyAlaPro between positions 90 and 115 and a constituent sequence TyrGlnXaaThrPro between positions 285 and 310, with position 1 of the amino acid sequence being the starting methionine, wherein the mutation is an amino acid replacement of the aspartate in the constituent sequence AspGlyXaaXaaXaaThrGlyAlaPro or an amino acid replacement of the tyrosine in the constituent sequence TyrGlnXaaThrPro.

Claim 2 (Previously Presented): A homoserine transsuccinylase as claimed in claim 1, wherein it exhibits a resistance toward SAM or L-methionine which is increased (increased Ki) at least 2-fold as compared with that of the wild type.

Claim 3 (Previously Presented): A homoserine transsuccinylase as claimed in claim 1, wherein it contains one of the mutations listed in Table 1.

Claim 4 (Previously Presented): A metA allele which encodes a homoserine transsuccinylase as claimed in claim 1.

Claim 5 (Previously Presented): A plasmid, wherein it contains a metA allele as claimed in claim 4 together with a promoter.

Claim 6 (Previously Presented): A microorganism strain, wherein it contains a feedback-resistant metA allele as claimed in claim 4.

Claim 7 (Previously Presented): A microorganism strain as claimed in claim 6, wherein it is a Gram-negative bacterial strain, preferably E. coli.

Claim 8 (currently amended): A method for preparing L-methionine or SAM by culturing a microorganism strain as claimed in claim 6~~—or—~~7.